OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/020,478

DATE: 01/02/2002
TIME: 11:19:18

Input Set : A:\RTS-0303 Sequence Listing.txt
Output Set: N:\CRF3\01022002\J020478.raw

Does Not Comply
Corrected Diskette Needed

```
      3 <110> APPLICANT: C. Frank Bennett
      4       Kenneth Dobie
      6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF B-CELL ASSOCIATED PROTEIN EXPRESSION
      8 <130> FILE REFERENCE: RTS-0303
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/020,478
C--> 10 <141> CURRENT FILING DATE: 2001-12-13
     10 <160> NUMBER OF SEQ ID NOS: 88
     13 <210> SEQ ID NO: 1
     14 <211> LENGTH: 20
     15 <212> TYPE: DNA
     16 <213> ORGANISM: Artificial Sequence
     18 <220> FEATURE:
     20 <223> OTHER INFORMATION: Antisense Oligonucleotide
     22 <400> SEQUENCE: 1                                                    20
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     26 <210> SEQ ID NO: 2
     27 <211> LENGTH: 20
     28 <212> TYPE: DNA
     29 <213> ORGANISM: Artificial Sequence
     31 <220> FEATURE:
     33 <223> OTHER INFORMATION: Antisense Oligonucleotide
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     36 atgcattctg cccccaagga
     39 <210> SEQ ID NO: 3
     40 <211> LENGTH: 1416
     41 <212> TYPE: DNA
     42 <213> ORGANISM: Homo sapiens
     44 <220> FEATURE:
     46 <220> FEATURE:  delete
     47 <221> NAME/KEY: CDS
     48 <222> LOCATION: (186)...(1085)
     50 <400> SEQUENCE: 3
     51 aagttccggt ccgtagtggg ctaaggggga gggtttcaaa gggagcgcac ttccgctgcc    60
     53 ctttctttcg ccagccttac gggcccgaac cctcgtgtga agggtgcagt acctaagccg   120
     55 gagcggggta gaggcgggcc ggcaccccct tctgacctcc agtgccgccg gcctcaagat   180
     57 cagac atg gcc cag aac ttg aag gac ttg gcg gga cgg ctg ccc gcc ggg   230
     58       Met Ala Gln Asn Leu Lys Asp Leu Ala Gly Arg Leu Pro Ala Gly
     59         1               5                  10                  15
     61 ccc cgg ggc atg ggc acg gcc ctg aag ctg ttg ctg ggg gcc ggc gcc    278
     62 Pro Arg Gly Met Gly Thr Ala Leu Lys Leu Leu Leu Gly Ala Gly Ala
     63                 20                  25                  30
     65 gtg gcc tac ggt gtg cgc gaa tct gtg ttc acc gtg gaa ggc ggg cac    326
     66 Val Ala Tyr Gly Val Arg Glu Ser Val Phe Thr Val Glu Gly Gly His
     67             35                  40                  45
     69 aga gcc atc ttc ttc aat cgg atc ggt gga gtg cag cag gac act atc    374
     70 Arg Ala Ile Phe Phe Asn Arg Ile Gly Gly Val Gln Gln Asp Thr Ile
     71         50                  55                  60
```

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73 ctg gcc gag ggc ctt cac ttc agg atc cct tgg ttc cag tac ccc att      422
74 Leu Ala Glu Gly Leu His Phe Arg Ile Pro Trp Phe Gln Tyr Pro Ile
75      65                  70                  75
77 atc tat gac att cgg gcc aga cct cga aaa atc tcc tcc cct aca ggc      470
78 Ile Tyr Asp Ile Arg Ala Arg Pro Arg Lys Ile Ser Ser Pro Thr Gly
79  80                  85                  90                  95
81 tcc aaa gac cta cag atg gtg aat atc tcc ctg cga gtg ttg tct cga      518
82 Ser Lys Asp Leu Gln Met Val Asn Ile Ser Leu Arg Val Leu Ser Arg
83                 100                 105                 110
85 ccc aat gct cag gag ctt cct agc atg tac cag cgc cta ggg ctg gac      566
86 Pro Asn Ala Gln Glu Leu Pro Ser Met Tyr Gln Arg Leu Gly Leu Asp
87             115                 120                 125
89 tac gag gaa cga gtg ttg ccg tcc att gtc aac gag gtg ctc aag agt      614
90 Tyr Glu Glu Arg Val Leu Pro Ser Ile Val Asn Glu Val Leu Lys Ser
91         130                 135                 140
93 gtg gtg gcc aag ttc aat gcc tca cag ctg atc acc cag cgg gcc cag      662
94 Val Val Ala Lys Phe Asn Ala Ser Gln Leu Ile Thr Gln Arg Ala Gln
95     145                 150                 155
97 gta tcc ctg ttg atc cgc cgg gag ctg aca gag agg gcc aag gac ttc      710
98 Val Ser Leu Leu Ile Arg Arg Glu Leu Thr Glu Arg Ala Lys Asp Phe
99 160                 165                 170                 175
101 agc ctc atc ctg gat gat gtg gcc atc aca gag ctg agc ttt agc cga     758
102 Ser Leu Ile Leu Asp Asp Val Ala Ile Thr Glu Leu Ser Phe Ser Arg
103                180                 185                 190
105 gag tac aca gct gct gta gaa gcc aaa caa gtg gcc cag cag gag gcc     806
106 Glu Tyr Thr Ala Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu Ala
107            195                 200                 205
109 cag cgg gcc caa ttc ttg gta gaa aaa gca aag cag gaa cag cgg cag     854
110 Gln Arg Ala Gln Phe Leu Val Glu Lys Ala Lys Gln Glu Gln Arg Gln
111        210                 215                 220
113 aaa att gtg cag gcc gag ggt gag gcc gag gct gcc aag atg ctt gga     902
114 Lys Ile Val Gln Ala Glu Gly Glu Ala Glu Ala Ala Lys Met Leu Gly
115    225                 230                 235
117 gaa gca ctg agc aag aac cct ggc tac atc aaa ctt cgc aag att cga     950
118 Glu Ala Leu Ser Lys Asn Pro Gly Tyr Ile Lys Leu Arg Lys Ile Arg
119 240                 245                 250                 255
121 gca gcc cag aat atc tcc aag acg atc gcc aca tca cag aat cgt atc     998
122 Ala Ala Gln Asn Ile Ser Lys Thr Ile Ala Thr Ser Gln Asn Arg Ile
123                260                 265                 270
125 tat ctc aca gct gac aac ctt gtg ctg aac cta cag gat gaa agt ttc    1046
126 Tyr Leu Thr Ala Asp Asn Leu Val Leu Asn Leu Gln Asp Glu Ser Phe
127            275                 280                 285
129 acc agg gga agt gac agc ctc atc aag ggt aag aaa tga gcctagtcac    1095
130 Thr Arg Gly Ser Asp Ser Leu Ile Lys Gly Lys Lys
131        290                 295
133 caagaactcc acccccagag gaagtggatc tgcttctcca gtttttgagg agccagccag  1155
135 gggtccagca cagccctacc ccgccccagt atcatgcgat ggtcccccac accggttccc  1215
137 tgaacccctc ttggattaag gaagactgaa gactagcccc ttttctggga aattactttc  1275
139 ctcctccctg tgttaactgg ggctgttggg gacagtgcgt gatttctcag tgatttccta  1335
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141 cagtgttgtt ccctccctca aggctgggag gagataaaca ccaacccagg aattctcaat 1395
143 aaatttttat tacttaacct g 1416
146 <210> SEQ ID NO: 4
147 <211> LENGTH: 21
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
153 <223> OTHER INFORMATION: PCR Primer
155 <400> SEQUENCE: 4 21
156 gcaagaaccc tggctacatc a
159 <210> SEQ ID NO: 5
160 <211> LENGTH: 20
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
166 <223> OTHER INFORMATION: PCR Primer
168 <400> SEQUENCE: 5 20
169 gtggcgatcg tcttggagat
172 <210> SEQ ID NO: 6
173 <211> LENGTH: 24
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
179 <223> OTHER INFORMATION: PCR Probe
181 <400> SEQUENCE: 6 24
182 acttcgcaag attcgagcag ccca
185 <210> SEQ ID NO: 7
186 <211> LENGTH: 19
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
192 <223> OTHER INFORMATION: PCR Primer
194 <400> SEQUENCE: 7 19
195 gaaggtgaag gtcggagtc
198 <210> SEQ ID NO: 8
199 <211> LENGTH: 20
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
205 <223> OTHER INFORMATION: PCR Primer
207 <400> SEQUENCE: 8 20
208 gaagatggtg atgggatttc
211 <210> SEQ ID NO: 9
212 <211> LENGTH: 20
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
218 <223> OTHER INFORMATION: PCR Probe
220 <400> SEQUENCE: 9

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20

221 caagcttccc gttctcagcc
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 6000
226 <212> TYPE: DNA
227 <213> ORGANISM: Homo sapiens
229 <220> FEATURE:
231 <221> NAME/KEY: intron
232 <222> LOCATION: (576)...(711)
233 <223> OTHER INFORMATION: intron 1
W--> 235 <221> NAME/KEY: exon:intron junction
236 <222> LOCATION: (796)...(797)
237 <223> OTHER INFORMATION: exon 2:intron 2
W--> 239 <221> NAME/KEY: intron:exon junction
240 <222> LOCATION: (1414)...(1415)
241 <223> OTHER INFORMATION: intron 2:exon 3
W--> 243 <221> NAME/KEY: exon:intron junction
244 <222> LOCATION: (1494)...(1495)
245 <223> OTHER INFORMATION: exon 3:intron 3
247 <221> NAME/KEY: intron
248 <222> LOCATION: (1495)...(2396)
249 <223> OTHER INFORMATION: intron 3
251 <221> NAME/KEY: exon
252 <222> LOCATION: (3213)...(3316)
253 <223> OTHER INFORMATION: exon 6
W--> 255 <221> NAME/KEY: exon:intron junction
256 <222> LOCATION: (3316)...(3317)
257 <223> OTHER INFORMATION: exon 6:intron 6
259 <221> NAME/KEY: intron
260 <222> LOCATION: (3317)...(3743)
261 <223> OTHER INFORMATION: intron 6
W--> 263 <221> NAME/KEY: intron:exon junction
264 <222> LOCATION: (5075)...(5076)
265 <223> OTHER INFORMATION: intron 8:exon 9
267 <400> SEQUENCE: 10
268 tcccagtcct gtgcctgctc cccaccgctt cgttcacgag gcttgaatcc atcactgggc 60
270 gcggccatct tgcaacaata ccggaagttg cgctaacgct cttaaataag aacagcgcgg 120
272 cttctaatca caaatttcct tccggctgcc attttgaaag tgggccagga aatggagatg 180
274 acttgctgtc ttgcgctgcc ctccctggga gggcagcctt ccagaaaggg gcgggacttc 240
276 cgtatgcgcg attcctgtgc gcgaagttcg ggtccgtagt gggctaaggg ggagggtttc 300
278 aaagggagcg cacttccgct gccctttctt tcgccagcct tacgggcccg aaccctcgtg 360
280 tgaaggggtgc agtacctaag ccggagcggg gtagaggcgg gccggcaccc ccttctgacc 420
282 tccagtgccg ccggcctcaa gatcagacat ggcccagaac ttgaaggact tggcgggacg 480
284 gctgcccgcc gggccccggg gcatgggcac ggccctgaag ctgttgctgg gggccggcgc 540
286 cgtggcctac ggtgtgcgcg aatctgtgtt caccggtgag caacctccgc ctgctcgccg 600
288 gacgcttcca gtccctcccc caaacccctt gccctgtccc cgcgcccctc cacgggccta 660
290 gcatttcctc tgagcagcgg cctggcctga tcaccaccca tctccccaca gtggaaggcg 720
292 ggcacagagc catcttcttc aatcggatcg gtggagtgca gcaggacact atcctggccg 780
294 agggccttca cttcaggtaa tggcgggcag agcctgctga ccctgacctt tcaccttga 840
296 cgccgaccca gcagtggcta tagtcggacg tgcaacagga ttcaacgctg ctcttttccc 900

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298 accctcctca tccctgcccc taggatagtg ggtgctgcga gaacctccag cagcatacaa   960
300 actgttgttt tccagaggga caagagaatc tctccttgtc tgtggtcgtg gagaggagca  1020
302 ggccaaaaaa cgcgtggtga ggggaaaccg ggcaaggcta gtgaaactgc ggccttttct  1080
304 ttttttttt ttggagaggg agtcttgctc tgtcgcccag gctggagtgc agtggcgcga  1140
306 tctcggctca ctgcaacctc cgcctcctga tttcaagcga ttctcctgcc tcagcctcac  1200
308 gagtagctgg gattacaggc gcccgccacc acgcccggct aatttttgta ttttagtaga  1260
310 gacggggttt cactatgtag atcaagctgg tctcgaactc ctgacctcaa atgatccgcc  1320
312 cgcctcggcc tcccaaagtg ctgggattac aggcgtgagc caccgcgccc ggccgaaact  1380
314 gtggcctctt aatacctatc cctgtcctct ccaggatccc ttggttccag taccccatta  1440
316 tctatgacat tcgggccaga cctcgaaaaa tctcctcccc tacaggctcc aaaggtaggt  1500
318 ctgagcactt ggtaatcaca tggcaggtgg gatgatcaag gtagctggca agaaacccca  1560
320 ggggaatatg gtagtgtcag gcctttaggc ctctttccac atctgcaaga gctgtaacaa  1620
322 aaatacctgc ctcctggggt caaagcagca aattctgaac acactgtgtt tgcgtgcttt  1680
324 ttactgtctc ctcoctgacg tgtattcaat aagagtattg tttgtcoctc gtcttgttca  1740
326 ctgcctagat caaagctttg ttttaaagcc ttttttttct aactgcttga cttactatat  1800
328 ctacagttac atccactagt acactctgtt ctggagaagt ttgtccctaa gcttgactag  1860
330 ttcacctgtt ctctccttct agaccataca taaaagccgt gcctttgagt tccccagacc  1920
332 tcttctcctc ccccacccac gcacacatat acaccctggg tcaggtagct cacctgtaac  1980
334 ctgtaatgta cttctttgtg ctatacctag tgcaggtcgc ttattcattt actagactgg  2040
336 gccctgggaa taaaagattc attaaacaca attcttgtcc cccaagtcct tacaggagac  2100
338 atgattacgg tacagcacga aagcgcccac gttagaggtt gcacagagta cagaggggga  2160
340 aagagtagtc agctctgctg gtgacggggt ttgcagttca agggttcaca gtgggtgagg  2220
342 gtgcatttca gctgtgctgc gtcttgtctt ccttgtcagc ctgattaact ctcctccccc  2280
344 cagggtagtg ccaggctgta caccattgca cagggcatac agggaggaac atgaaggaga  2340
346 aaatgcttgg gaaagggtgt ttggccttga ccagccactg ctgacctcaa tctcagacct  2400
348 acagatggtg aatatctccc tgcgagtgtt gtctcgaccc aatgctcagg agcttcctag  2460
350 catgtaccag cgcctagggc tggactacga ggaacgagtg ttgccgtcca ttgtcaacga  2520
352 ggtgctcaag agtgtggtgg ccaagttcaa tgcctcacag ctgatcaccc agcgggccca  2580
354 ggtctgactc ccaccaccat ctgcgtggtg tcagcctttc cttcctaggc ccagagtatt  2640
356 gggaattagg aaaggcagct tattagaaaa gcattgtcac cctagtgcca tttccacctc  2700
358 aaagctgtgc taattgccac tgtgaaataa ggagagccag cattagaact cgatagcact  2760
360 cggtgttagg aagcacagag gaaaatggcc aagtcttggc ttttcctgca cctcttcgag  2820
362 cagagaggct tatgttacag gtttgcctga caggaagcta aggcagtgca tgttgtattg  2880
364 agagtgaagg gttaggggtc gcaaccttcc tttcagctcc ccagtcccct caaaccaccc  2940
366 ctccctccc ctcttcaccc ctgccctcag gtatccctgt tgatccgccg ggagctgaca  3000
368 gagagggcca aggacttcag cctcatcctg gatgatgtgg ccatcacaga gctgagcttt  3060
370 agccgagagt acacagctgc tgtagaagcc aaacaagtgg gtgagtcgca agagccgtgg  3120
372 ggtgagggct tctgagatgc aggaggagga aagactccat gggtgggct cctgacccag  3180
374 gacagggtct ccctgactct ctcccaccac agcccagcag gaggcccagc gggcccaatt  3240
376 cttggtagaa aaagcaaagc aggaacagcg gcagaaaatt gtgcaggccg agggtgaggc  3300
378 cgaggctgcc aagatgatat ccttctgctg gagagatctc agcccagccc ctagggcacc  3360
380 tgagttcccc attctccttc atgggcaggc tgatgagact aaggcgaatg cgactccgtg  3420
382 ctctctggcc cttggctcct tgttgggggt ggggactaca gatgagatct gaaatcttag  3480
384 tggtagtacc tgagccatga ctccccactg taaggccaga tcaatagcat tggtggcctt  3540
386 gccttcattt ctggtgctgc ccctagttcc tggcagcagc ctgcagggag gcccacaggt  3600
388 ggggtccacg gtagggctgg gcacaagcca cctgagcgca accttggatc tgacagccca  3660
390 gaggaggact ggagcaaggg agtgtggtaa ggacagggcc agggattgag acctgccctt  3720
392 gcgtgtacct taaccctcct caccttggag aagcactgag caagaaccct ggctacatca  3780
394 aacttcgcaa gattcgagca gcccagaata tctccaagac ggtgagtgtg tcagcccagc  3840
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:235 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:239 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:243 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:255 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:263 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10